

## CLAIMS AS FILED - OZ 50815

1. An isolated nucleic acid sequence which encodes a polypeptide and which is composed of a combination of the nucleic acid sequences of a biosynthesis nucleic acid sequence of the fatty acid or lipid metabolism and one of the following nucleic acids:
  - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,
  - b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,
  - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
  - d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence.
2. An isolated nucleic acid sequence as claimed in claim 1, wherein a sequence of the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism:

Acyl-CoA dehydrogenase(s), Acyl-ACP [= acyl carrier protein] desaturase(s), Acyl-ACP thioesterase(s), fatty acid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases and/or fatty acid elongase(s).
3. An isolated nucleic acid sequence as claimed in claim 1, wherein a sequence of

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the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism:

fatty acid acyltransferase(s),  $\Delta 4$  desaturase,  $\Delta 5$  desaturase,  $\Delta 6$  desaturase,  $\Delta 9$  desaturase,  $\Delta 12$  desaturase,  $\Delta 15$  desaturase or a fatty acid elongase.

4. An isolated nucleic acid sequence as claimed in claim 1, wherein the derivatives mentioned under (c) have a homology at the amino acid level of 70%, preferably 80%, especially preferably of 90%, over the entire region of the sequence shown in SEQ ID NO: 2 (Program PileUp, J. Mol. Evolution., 25, 351-360, 1987, Higgins et al., CABIOS, 5 1989: 151-153).
5. An amino acid sequence encoded by a nucleic acid sequence as claimed in claim 1.
6. A nucleic acid construct comprising a nucleic acid sequence as claimed in claim 1, wherein the nucleic acid sequence is linked to one or more regulatory signals.
7. The use of a nucleic acid sequence as claimed in claim 1 or of a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals for the generation of transgenic plants.
8. A vector comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals.
9. A vector as claimed in claim 8, which is a linear or circular DNA, a phage, a virus,

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- a transposon, an IS element, a phasmid, a phagemid, a cosmid or a plasmid.
10. An organism comprising at least one nucleic acid sequence as claimed in claim 1, at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals or at least one vector comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals or a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals.
  11. An organism as claimed in claim 10, which is a eukaryotic organism.
  12. An organism as claimed in claim 10, which is a plant, a eukaryotic microorganism or an animal.
  13. An organism as claimed in claim 10, which is a plant, a fungus or a yeast.
  14. An organism as claimed in claim 10, which is *Yarrowia lypolytica*, *Saccharomyces cerevisiae*, *Traustochytrium*, *Arabidopsis thaliana*, *Brassica napus* or *Linum usitatissimum*.
  15. A transgenic plant comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct comprising said nucleic acid sequence.
  16. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises combining the protein-encoding nucleic acids and one of the following sequences to give a joint protein-encoding sequence:
    - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,

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- b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,
  - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
  - d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence, and introducing the resulting sequence into a eukaryotic organism.
17. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism.
18. A method of producing fatty acids or lipids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism, growing this organism and isolating the oil contained in the organism.
19. A method of producing fatty acids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism, growing this

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organism, isolating the oil contained in the organism and liberating the fatty acids.

20. A method as claimed in claim 16, wherein the organism is a plant or a eukaryotic microorganism.